

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 31, 2005, 18:10:30 ; Search time 28 Seconds
(without alignments)
48.108 Million cell updates/sec

Title: US-10-083-768-12

Perfect score: 85

Sequence: 1 CADGPTLREWISFC 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	52.9	108	2 T49731	hypothetical prote
2	44	51.8	974	2 S34189	starch phosphoryla
3	44	51.8	1022	1 S00503	Na+/K+-exchanging
4	44	51.8	1023	2 A24414	Na+/K+-exchanging
5	43	50.6	245	2 T47701	translation initia
6	43	50.6	490	2 T09084	phosphatidylinosit
7	43	50.6	1010	2 B37227	Na+/K+-exchanging
8	43	50.6	1013	1 S00801	Na+/K+-exchanging
9	43	50.6	1013	2 C24639	Na+/K+-exchanging
10	43	50.6	1017	2 A37227	Na+/K+-exchanging
11	43	50.6	1020	2 A34474	Na+/K+-exchanging
12	43	50.6	1020	2 B24639	Na+/K+-exchanging
13	43	50.6	1021	1 PWSHNA	Na+/K+-exchanging
14	43	50.6	1021	1 S04630	Na+/K+-exchanging
15	43	50.6	1021	2 A28199	Na+/K+-exchanging
16	43	50.6	1021	2 B24862	Na+/K+-exchanging
17	43	50.6	1022	2 S49127	Na+/K+-exchanging
18	43	50.6	1023	1 A24639	Na+/K+-exchanging
19	43	50.6	1023	1 S24650	Na+/K+-exchanging
20	43	50.6	1025	2 A60444	Na+/K+-exchanging
21	43	50.6	1027	1 PWCNNM	Na+/K+-exchanging
22	43	50.6	1038	1 S03632	Na+/K+-exchanging
23	42.5	50.0	1004	2 JH0470	Na+/K+-exchanging
24	42	49.4	312	2 F86876	hypothetical prote
25	42	49.4	522	2 D69226	hypothetical prote
26	42	49.4	522	2 S62941	probable membrane
27	42	49.4	725	2 A11544	conserved hypothet
28	42	49.4	842	2 T12091	starch phosphoryla
29	41	48.2	189	2 S07755	hypothetical prote

ALIGNMENTS

RESULT 1

T49731

hypothetical protein B24B19.30 [imported] - Neurospora crassa

C:Species: Neurospora crassa

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000

C:Accession: T49731

R:Schulze, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,

submitted to the Protein Sequence Database, May 2000

A:Reference number: 225022

A:Accession: T49731

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-108 <SCH>

A:Cross-references: EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.30

A:Experimental source: BAC clone B24B19; strain OR74A

C:Genetics:

A:Gene: NCSP:B24B19.30

A:Map position: 6

C:Superfamily: Neurospora crassa hypothetical protein B24B19.30

Query Match 52.9%; Score 45; DB 2; Length 108;
Best Local Similarity 50.0%; Pred. No. 3.6;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CADGPTLREWISFC 14

Db 70 CQCQPILRNWLSWC 83

RESULT 2

S34189

starch phosphorylase (EC 2.4.1.1) L - potato

C:Species: Solanum tuberosum (potato)

C>Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S53489; S34189

R:Sonnefeld, U.; Basner, A.; Greve, B.; Steup, M.

Plant Mol. Biol. 27, 567-576, 1995

A:Title: A second L-type isozyme of potato glucan phosphorylase: cloning, antisense inhi

A:Reference number: S53489; MUID:95201249; PMID:7894019

A:Accession: S53489

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-974 <S02>

A:Cross-references: UNIPROT:P53535; EMBL:X73684; NID:g313348; PIDN:CAA52036.1; PID:g31333

C:Superfamily: glucan phosphorylase

C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein; pyridoxal phosphate

F;820/Binding site: pyridoxal phosphate [Lys] (covalent) #status predicted

Query Match 51.8%; Score 44; DB 2; Length 974;

Best Local Similarity 58.3%; Pred. No. 43;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 DGPTRLREWISFC 14
: |||||
Db 619 NGVTPRWLSFC 630

RESULT 3
S00503
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - Pacific electric ray
C:Species: Torpedo californica (Pacific electric ray)
C:Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: S00503; S28885; S28880
R:Kawakami, K.; Noguchi, S.; Noda, M.; Takahashi, H.; Ohta, T.; Kawamura, M.; Nojima, H.
Nature 316, 733-736, 1985
A:Title: Primary structure of the alpha-subunit of Torpedo californica (Na(+)+K(+))ATPase
A:Reference number: S00503; MUID:85296307; PMID:2993905
A:Accession: S00503
A:Molecule type: mRNA
A:Residues: 1-1022 <KAW1>
A:Cross-references: UNIPROT:P05025; EMBL:X02810; NID:G643399; PIDN:CAA26578.1; PID:G64400
A:Accession: S28885
A:Molecule type: protein
A:Residues: 228-240/431-438;535-550;671-690;1011-1022 <KAW2>
R:Ohta, T.; Nagano, K.; Yoshida, M.
Proc. Natl. Acad. Sci. U.S.A. 83, 2071-2075, 1986
A:Title: The active site structure of Na(+)/K(+)-transporting ATPase: location of the 5'
A:Reference number: S29880; MUID:86177549; PMID:3008150
A:Accession: S29880
A:Molecule type: protein
A:Residues: 386-402/502-512;671-689;887-906 <OHT>
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F:96-120/Domain: transmembrane #status predicted <TM1>
F:130-149/Domain: transmembrane #status predicted <TM2>
F:150-290/Domain: intracellular #status predicted <TM3>
F:291-313/Domain: transmembrane #status predicted <TM2>
F:320-348/Domain: transmembrane #status predicted <TM4>
F:349-785/Domain: intracellular #status predicted <INT3>
F:586-782/Domain: intracellular #status predicted <INT3>
F:786-809/Domain: transmembrane #status predicted <TM5>
F:848-873/Domain: transmembrane #status predicted <TM6>
F:874-951/Domain: intracellular #status predicted <INT4>
F:952-977/Domain: transmembrane #status predicted <TM7>
F:978-1022/Domain: extracellular #status predicted <EXT>
F:376/Active site: Asp (aspartylphosphate intermediate) #status predicted
F:507/Binding site: ATP (Lys) #status predicted
F:716,720,725/Active site: Asp, Asp, Lys #status predicted

QY 5 PTLREWISFC 14
: |||||
Db 84 PTPPEWIKFC 93

RESULT 4
A24414
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - human
N:Alternate names: sodium pump; sodium/potassium transporting ATPase alpha-A chain
C:Species: Homo sapiens (man)
C:Date: 02-Jun-1988 #sequence revision 02-Jun-1988 #text_change 09-Jul-2004
C:Accession: A24414; A27795; A39910; I60116; S09171
R:Kawakami, K.; Ohta, T.; Nojima, H.; Negano, K.
J. Biochem. 100, 389-397, 1986
A:Title: Primary structure of the alpha-subunit of human Na,K-ATPase deduced from cDNA s
A:Reference number: A24414; MUID:87057096; PMID:2430951
A:Accession: A24414
A:Molecule type: mRNA
A:Residues: 1-1023 <KAW>
A:Cross-references: UNIPROT:P05023; EMBL:X04297; NID:G28926; PIDN:CAA27840.1; PID:G28927
R:Shull, M.M.; Lingrel, J.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987

A:Title: Multiple genes encode the human Na+,K+-ATPase catalytic subunit.
A:Reference number: A94158; MUID:87231946; PMID:3035563
A:Accession: A27795
A:Molecule type: DNA
A:Residues: 168-189;213-214,'X',216-244 <SHU>
R:Chehab, F.F.; Kan, Y.W.; Law, M.L.; Hartz, J.; Kao, F.T.; Blostein, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7901-7905, 1987
A:Title: Human placental Na+,K+-ATPase alpha subunit: cDNA cloning, tissue expression, DN
A:Reference number: A39910; MUID:88068506; PMID:2891135
A:Accession: A39910
A:Molecule type: mRNA
A:Residues: 199-942 <CHE>
R:Shull, M.M.; Pugh, D.G.; Lingrel, J.B.
Genomics 6, 451-460, 1990
A:Title: The human Na, K-ATPase alpha 1 gene: characterization of the 5'-flanking region
A:Reference number: I60116; MUID:90228961; PMID:1970326
A:Accession: I60116
A:Status: translation not shown; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-61 <RES>
A:Cross-references: GB:M30310; NID:G179206; PIDN:AAAS1801.1; PID:G179208
C:Genetics:
A:Gene: GDB:ATP1A1
A:Map Position: 1p13-lp11
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein; i
F:6-1023/Domain: intracellular #status predicted <INT1>
F:96-120/Domain: transmembrane #status predicted <TM1>
F:130-149/Domain: transmembrane #status predicted <TM2>
F:150-290/Domain: intracellular #status predicted <TM3>
F:291-313/Domain: transmembrane #status predicted <TM4>
F:320-348/Domain: transmembrane #status predicted <TM4>
F:349-786/Domain: intracellular #status predicted <INT3>
F:587-783/Domain: ATPase nucleotide-binding domain homology <ATN>
F:787-810/Domain: transmembrane #status predicted <TM5>
F:849-874/Domain: transmembrane #status predicted <TM6>
F:875-952/Domain: intracellular #status predicted <TM7>
F:953-978/Domain: transmembrane #status predicted <TM7>
F:979-1023/Domain: extracellular #status predicted <EXT>
F:376/Active site: Asp (aspartylphosphate intermediate) #status predicted
F:508/Binding site: ATP (Lys) #status predicted
F:717,721,726/Active site: Asp, Asp, Lys #status predicted

Query Match 51.8%; Score 44; DB 2; Length 1023;
Best Local Similarity 70.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTLREWISFC 14
: |||||
Db 84 PTPPEWIKFC 93

RESULT 5
T47701
translation initiation factor eIF-6-like protein [imported] - Arabidopsis thaliana
N:Alternate names: protein F116.30
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47701
R:Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24473
A:Accession: T47701
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-245 <BEN>
A:Cross-references: UNIPROT:Q9M060; EMBL:AL161667
A:Experimental source: cultivar Columbia; BAC clone F1116
C:Genetics:

R;Shull, G.E.; Greeb, J.; Lingrel, J.B.
Biochemistry 25, 8125-8132, 1986
A;Title: Molecular cloning of three distinct forms of the Na⁺, K⁺-ATPase alpha-subunit from chicken erythrocytes
A;Reference numbers: A30512; MUID:87128908; PMID:3028470
A;Accession: C24639
A;Molecule type: mRNA
A;Residues: 1-1013 <SHU>
A;Cross-references: UNIPROT:P06587; EMBL:M14513; NID:G203030; PIDN:AAA40777.1; PID:G203030
A;Note: In the authors' translation 405-Ser is shown after residue 409 and, consequently, the residue numbering is shifted by one position.
R;Hara, Y.; Urayama, O.; Kawakami, K.; Nojima, H.; Nagamune, H.; Kojima, T.; Ohka, T.; Nishida, K.; Lingrel, J.B.
J. Biochem. 102, 43-58, 1987
A;Title: Primary structures of two types of alpha-subunit of rat brain Na⁺, K⁺-ATPase
A;Reference number: S00460; MUID:88032933; PMID:2822682
A;Accession: S00514
A;Molecule type: mRNA
A;Residues: 1-907, 'C', 909-1013 <HAR>
A;Cross-references: EMBL:X05883; NID:G55769; PIDN:CAA29307.1; PID:G55770
R;Herrera, V.L.M.; Emanuel, J.R.; Ruiz-Opazo, N.; Levenson, R.; Nadal-Ginard, B.
J. Cell Biol. 105, 1855-1865, 1987
A;Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural analysis and localization of the alpha-2 and alpha-3 isoforms
A;Reference number: A92749; MUID:88033255; PMID:2822726
A;Accession: B27180
A;Molecule type: mRNA
A;Residues: 1, 'NL', 4-103, 'R', 105-113, 'E', 115-127, 'G', 129-148, 'Q', 150-151, 'T', 153-165, 'D', 167-177, 'S', 181-189, 'S', 191-199, 'S', 201-209, 'S', 211-219, 'S', 221-229, 'S', 231-239, 'S', 241-249, 'S', 251-259, 'S', 261-269, 'S', 271-279, 'S', 281-289, 'S', 291-299, 'S', 301-309, 'S', 311-319, 'S', 321-329, 'S', 331-339, 'S', 341-349, 'S', 351-359, 'S', 361-369, 'S', 371-379, 'S', 381-389, 'S', 391-399, 'S', 401-409, 'S', 411-419, 'S', 421-429, 'S', 431-439, 'S', 441-449, 'S', 451-459, 'S', 461-469, 'S', 471-479, 'S', 481-489, 'S', 491-499, 'S', 501-509, 'S', 511-519, 'S', 521-529, 'S', 531-539, 'S', 541-549, 'S', 551-559, 'S', 561-569, 'S', 571-579, 'S', 581-589, 'S', 591-599, 'S', 601-609, 'S', 611-619, 'S', 621-629, 'S', 631-639, 'S', 641-649, 'S', 651-659, 'S', 661-669, 'S', 671-679, 'S', 681-689, 'S', 691-699, 'S', 701-709, 'S', 711-719, 'S', 721-729, 'S', 731-739, 'S', 741-749, 'S', 751-759, 'S', 761-769, 'S', 771-779, 'S', 781-789, 'S', 791-799, 'S', 801-809, 'S', 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F;584-780/Domain: ATPase nucleotide-binding domain homology <ATN>
F;784-807/Domain: transmembrane #status predicted <TM5>
F;846-871/Domain: transmembrane #status predicted <TM6>
F;872-949/Domain: intracellular #status predicted <INT4>
F;950-975/Domain: transmembrane #status predicted <TM7>
F;976-1020/Domain: extracellular #status predicted <EXT>
F;374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F;505/Binding site: ATP (lys) #status predicted
F;714,718,723/Active site: Asp, Asp, Lys #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1020;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PTLREWISFC 14
Db 82 PTPPEWVKFC 91

RESULT 12
B24639
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-2 chain - rat
N/Alternate names: Na+/K+-transporting ATPase alpha-plus chain
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C/Accession: B24639
R;Shull, G.E.; Greeb, J.; Lingrel, J.B.
Biochemistry 25, 8125-8132, 1986
A/Title: Molecular cloning of three distinct forms of the Na+,K+-ATPase alpha-subunit from sheep
A/Reference number: A90512; MUID:87128908; PMID:3028470
A/Accession: B24639
A/Molecule type: mRNA
A/Residues: 1-1020 <SHU>
A/Cross-references: UNIPROT:P06686; EMBL:M14512; NID:g203028; PIDN:AAA40776.1; PID:g203028
C/Genetics:
A/Gene: NKAA2
C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C/Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transport
F;6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MAT>
F;6-93/Domain: intracellular #status predicted <INT1>
F;94-119/Domain: transmembrane #status predicted <TM1>
F;128-147/Domain: transmembrane #status predicted <TM2>
F;148-288/Domain: intracellular #status predicted <INT2>
F;289-311/Domain: transmembrane #status predicted <TM3>
F;318-346/Domain: transmembrane #status predicted <TM4>
F;347-783/Domain: intracellular #status predicted <INT3>
F;584-780/Domain: ATPase nucleotide-binding domain homology <ATN>
F;784-807/Domain: transmembrane #status predicted <TM5>
F;846-871/Domain: transmembrane #status predicted <TM6>
F;872-949/Domain: intracellular #status predicted <INT4>
F;950-975/Domain: transmembrane #status predicted <TM7>
F;976-1020/Domain: extracellular #status predicted <EXT>
F;374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F;505/Binding site: ATP (lys) #status predicted
F;714,718,723/Active site: Asp, Asp, Lys #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1020;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PTLREWISFC 14
Db 82 PTPPEWVKFC 91

RESULT 13
PWSHNA
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain precursor - sheep
N/Alternate names: sodium pump alpha chain; sodium/potassium-dependent ATPase alpha chain
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C/Accession: A01074; A35426
R;Shull, G.E.; Schwartz, A.; Lingrel, J.B.

Nature 316, 691-695, 1985
A/Title: Amino-acid sequence of the catalytic subunit of the (Na(+)+K(+)) ATPase deduced from complementary DNA
A/Reference number: A01074; MUID:85296299; PMID:2993903
A/Accession: A01074
A/Molecule type: mRNA
A/Residues: 1-1021 <SHU>
A/Cross-references: UNIPROT:P04074; GB:X02813; NID:g1205; PIDN:CAA26581.1; PID:g1206
R;Hinz, H.R.; Kiriely, T.L.
J. Biol. Chem. 265, 10260-10265, 1990
A/Title: Lysozyme 480 is an essential residue in the putative ATP site of lamb kidney (Na, K)-ATPase
A/Reference number: A35426; MUID:90285144; PMID:2162343
A/Accession: A35426
A/Status: preliminary
A/Molecule type: protein
A/Residues: 475-492 <HIN>
C/Comment: This is the catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP to ADP and inorganic phosphate, providing the energy for active transport of Na+ and K+ across the cell membrane.
C/Comment: This enzyme is specifically inhibited by cardiac glycosides such as digoxin and ouabain.
C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C/Keywords: ATP; hydrolase; phosphoprotein; potassium transport; sodium transport; transport
F;6-1021/Product: Na+/K+-transporting ATPase alpha chain #status predicted <MAT>
F;94-115/Domain: transmembrane #status predicted <TM1>
F;128-144/Domain: transmembrane #status predicted <TM2>
F;289-311/Domain: transmembrane #status predicted <TM3>
F;318-346/Domain: transmembrane #status predicted <TM4>
F;585-781/Domain: ATPase nucleotide-binding domain homology <ATN>
F;785-808/Domain: transmembrane #status predicted <TM5>
F;847-976/Domain: transmembrane #status predicted <TM6>
F;951-972/Domain: transmembrane #status predicted <TM7>
F;315/Binding site: cardiac glycoside (Trp) #status predicted
F;374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F;506/Binding site: ATP (Lys) #status predicted

Query Match 50.6%; Score 43; DB 1; Length 1021;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PTLREWISFC 14
Db 82 PTPPEWVKFC 91

RESULT 14
S04630
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - horse
C/Species: Equus caballus (domestic horse)
C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C/Accession: S04630
R;Kano, I.; Nagai, F.; Satoh, K.; Ushiyama, K.; Nakao, T.; Kano, K.
FEBS Lett. 250, 91-98, 1989
A/Title: Structure of the alpha(1) subunit of horse Na,K-ATPase gene.
A/Reference number: S04630; MUID:89290042; PMID:2544461
A/Accession: S04630
A/Molecule type: DNA
A/Residues: 1-1021 <KAN>
A/Cross-references: UNIPROT:P18907; EMBL:X16773; NID:g1010; PIDN:CAA34716.1; PID:9871026
C/Genetics:
A/Introns: 4/3; 39/3; 59/3; 127/3; 165/3; 210/3; 250/3; 339/3; 406/3; 442/3; 487/3; 552/3; 585/3
C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C/Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transport
F;6-1021/Product: Na+/K+-transporting ATPase alpha-1 chain #status predicted <MAT>
F;6-93/Domain: intracellular #status predicted <INT1>
F;94-118/Domain: transmembrane #status predicted <TM1>
F;128-147/Domain: transmembrane #status predicted <TM2>
F;148-288/Domain: intracellular #status predicted <INT2>
F;289-311/Domain: transmembrane #status predicted <TM3>
F;318-346/Domain: transmembrane #status predicted <TM4>
F;347-784/Domain: intracellular #status predicted <INT3>
F;585-781/Domain: transmembrane #status predicted <TM5>
F;785-808/Domain: transmembrane #status predicted <TM6>
F;847-872/Domain: transmembrane #status predicted <TM6>
F;873-950/Domain: intracellular #status predicted <INT4>

F:951-976/Domain: transmembrane #status predicted <TM7>
F:977-1021/Domain: extracellular #status predicted <EXT>
F:374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F:506/Binding site: ATP (lys) #status predicted
F:715,719,724/Active site: Asp, Asp, Lys #status predicted

Query Match 50.6%; Score 43; DB 1; Length 1021;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PTLREWISFC 14
Db 82 PTPPEWVKFC 91

RESULT 15
A28199
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - chicken
C:Species: Gallus gallus (chicken)
C:Date: 21-Sep-1988 #sequence_revision 21-Sep-1988 #text_change 09-Jul-2004
C:Accession: A28199
R:Takeyasu, K.; Tamkun, M.M.; Renaud, K.J.; Fambrough, D.M.
J. Biol. Chem. 263, 4347-4354, 1988
A:Title: Ouabain-sensitive (Na(+) + K(+))-ATPase activity expressed in mouse L cells by
A:Reference number: A28199; MOID:88153759; PMID:2831227
A:Accession: A28199
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1021 <TAK>
A:Cross-references: UNIPROT:P09572; GB:J03230; NID:g211219; PIDN:AAA48607.1; PID:g211220
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; transmembrane protein
F:585-781/Domain: ATPase nucleotide-binding domain homology <ATN>
F:213,481/Binding site: carboxylate (Asn) (covalent) #status predicted
F:374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F:506/Binding site: ATP (Lys) #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1021;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PTLREWISFC 14
Db 82 PTPPEWVKFC 91

Search completed: January 31, 2005, 18:22:36
Job time : 30 secs